
Sequence Listing was accepted.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)

217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: Fri Sep 28 17:41:25 EDT 2007

Validated By CRFValidator v 1.0.3

Application No: 10758524 Version No: 2.0

Input Set:

Output Set:

Started: 2007-09-14 11:27:42.124 **Finished:** 2007-09-14 11:27:46.606

Elapsed: 0 hr(s) 0 min(s) 4 sec(s) 482 ms

Total Warnings: 53

Total Errors: 4

No. of SeqIDs Defined: 59

Actual SeqID Count: 59

Error code		Error Description
W	213	Artificial or Unknown found in <213> in SEQ ID (7)
W	213	Artificial or Unknown found in <213> in SEQ ID (8)
E	224	<220>, $<223>$ section required as $<213>$ has Artificial sequence or Unknown in SEQID (8)
Ε	341	'Xaa' position not defined SEQID (8) POS (439)
W	213	Artificial or Unknown found in <213> in SEQ ID (9)
W	213	Artificial or Unknown found in <213> in SEQ ID (10)
W	213	Artificial or Unknown found in <213> in SEQ ID (11)
W	213	Artificial or Unknown found in <213> in SEQ ID (12)
W	213	Artificial or Unknown found in <213> in SEQ ID (13)
W	213	Artificial or Unknown found in <213> in SEQ ID (14)
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W	213	Artificial or Unknown found in <213> in SEQ ID (16)
W	213	Artificial or Unknown found in <213> in SEQ ID (17)
W	213	Artificial or Unknown found in <213> in SEQ ID (18)
W	213	Artificial or Unknown found in <213> in SEQ ID (19)
W	213	Artificial or Unknown found in <213> in SEQ ID (20)
W	213	Artificial or Unknown found in <213> in SEQ ID (21)
W	213	Artificial or Unknown found in <213> in SEQ ID (22)
W	213	Artificial or Unknown found in <213> in SEQ ID (23)

Input Set:

Output Set:

Started: 2007-09-14 11:27:42.124 **Finished:** 2007-09-14 11:27:46.606

Elapsed: 0 hr(s) 0 min(s) 4 sec(s) 482 ms

Total Warnings: 53

Total Errors: 4

No. of SeqIDs Defined: 59

Actual SeqID Count: 59

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (24)
W 213	Artificial or Unknown found in <213> in SEQ ID (25)
W 213	Artificial or Unknown found in <213> in SEQ ID (26) This error has occured more than 20 times, will not be displayed
E 341	'Xaa' position not defined SEQID (26) POS (502)
E 341	'Xaa' position not defined SEQID (30) POS (502)

SEQUENCE LISTING

<110> Jaworski, Jan G. Blacklock, Brenda J. <120> FATTY ACID ELONGASE 3-KETOACYL COA SYNTHASE POLYPEPTIDES <130> 07148-108002 <140> 10758524 <141> 2004-01-15 <150> 09/877,476 <151> 2001-06-08 <150> 60/210,326 <151> 2000-06-08 <160> 59 <170> FastSEQ for Windows Version 4.0 <210> 1 <211> 1709 <212> DNA <213> Arabidopsis thaliana <220> <221> CDS <222> (1)...(1518) <400> 1 atg acg tcc gtt aac gtt aag ctc ctt tac cgt tac gtc tta acc aac 48 Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn 1 10 ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc gcc gga aaa 96 Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys 20 gcc tct cgg ctt acc ata aac gat ctc cac aac ttc ctt tcc tat ctc 144 Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu caa cac aac ctt ata aca gta act tta ctc ttt gct ttc act gtt ttc 192 Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe 50 55 60 ggt ttg gtt ctc tac atc gta acc cga ccc aat ccg gtt tat ctc gtt 240 Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val 65 70 75 288 gac tac tcg tgt tac ctt cca cca ccg cat ctc aaa gtt agt gtc tct Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Leu Lys Val Ser Val Ser

90

95

85

aaa gto	atg g	at att	ttc	tac	caa	ata	aga	aaa	gct	gat	act	tct	tca	336
Lys Val		sp Ile 00	Phe	Tyr	Gln	Ile 105	Arg	Lys	Ala	Asp	Thr 110	Ser	Ser	
cgg aac Arg Asr	2 2 2		_	_	_		_		_		_		-	384
att caa Ile Glr 130	Glu A													432
ctc att Leu Ile 145	_		_		-			-			-	-		480
aca gaç Thr Glı							-							528
aaa gtt Lys Val	. Asn P	-										-	-	576
ttt aat Phe Asr			_			-	_	-	_				-	624
ctc cga Leu Arc	Ser A			-						_		-	_	672
gct ggt Ala Gly 225				Asp										720
aaa aac Lys Asr		_				_								768
att tat Ile Tyr	Ala G			_		_	_	-	_		-	_		816
cgt gtt Arg Val					_				_	_		-		864
aga cgg Arg Arg 290	Ser L	-	_		-		_	-	_	_				912
gct gat Ala Asp 305	=	=		_	_				_	_	-		=	960

ggc aaa atc		-	-	_		1008
aca aca ctt	-	-				1056
tta agc gaa Leu Ser Glu 355	3	_	-	, ,		1104
cta aag gat Leu Lys Asp 370	_		Val Pro A	-	-	1152
gtt gac cat Val Asp His 385	_					1200
cta gag aag Leu Glu Lys					_	1248
tca acg tta Ser Thr Leu	_			=		1296
gaa tta gca Glu Leu Ala 435			-			1344
gct tgg cag Ala Trp Gln 450			Phe Lys C	_		1392
tgg gtg gct Trp Val Ala 465	-			-		1440
cat tgc atc			=		_	1488
tca aag act Ser Lys Thr	_			tgatg tatct	gagtg	1538
ccaacgttta c tcctctcttt t ttaagcgttt c	tcgttataa a	taaagaagt tc	aattcttc c	ctatagtttc a	ıaacgcgatt	1598 1658 1709
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Ala	Ser	Arg 35	Leu	Thr	Ile	Asn	Asp 40	Leu	His	Asn	Phe	Leu 45	Ser	Tyr	Leu
Gln	His 50	Asn	Leu	Ile	Thr	Val 55	Thr	Leu	Leu	Phe	Ala 60	Phe	Thr	Val	Phe
_	Leu	Val	Leu	Tyr		Val	Thr	Arg	Pro		Pro	Val	Tyr	Leu	
65					70					75					80
Asp	Tyr	Ser	Cys	Tyr 85	Leu	Pro	Pro	Pro	His 90	Leu	Lys	Val	Ser	Val 95	Ser
Lys	Val	Met	Asp 100	Ile	Phe	Tyr	Gln	Ile 105	Arg	Lys	Ala	Asp	Thr 110	Ser	Ser
Arg	Asn	Val 115	Ala	Cys	Asp	Asp	Pro 120	Ser	Ser	Leu	Asp	Phe 125	Leu	Arg	Lys
Ile			Arg	Ser	Gly	Leu		Asp	Glu	Thr	Tyr		Pro	Glu	Gly
	130					135					140				
Leu	Ile	His	Val	Pro	Pro	Arg	Lys	Thr	Phe	Ala	Ala	Ser	Arg	Glu	Glu
145					150					155					160
Thr	Glu	Lys	Val		Ile	Gly	Ala	Leu		Asn	Leu	Phe	Glu		Thr
_		_	_	165		- 1	1		170				_	175	
Lys	Val	Asn		Arg	Glu	Ile	GLy		Leu	Val	Val	Asn		Ser	Met
DI.	7	D	180	D	G	T	a	185	N.F L	T7 - 3	T7 - 7	7	190	DI.	T
		195				Leu	200					205			_
Leu	Arg 210	Ser	Asn	Ile	Lys	Ser 215	Phe	Asn	Leu	Gly	Gly 220	Met	Gly	Cys	Ser
Ala 225	Gly	Val	Ile	Ala	Ile 230	Asp	Leu	Ala	Lys	Asp 235	Leu	Leu	His	Val	His 240
	Asn	Thr	Tur	Δla		Val	Val	Ser	Thr		Asn	Tle	Thr	Gln	
_			_	245					250					255	_
116	ıyr	Ala	260	GIU	Asn	Arg	ser	265	Met	vai	ser	Asn	270	Leu	Pne
Arg	Val	Gly 275	Gly	Ala	Ala	Ile	Leu 280	Leu	Ser	Asn	Lys	Ser 285	Gly	Asp	Arg
Arg	Arg 290	Ser	Lys	Tyr	Lys	Leu 295	Val	His	Thr	Val	Arg 300	Thr	His	Thr	Gly
Ala	Asp	Asp	Lys	Ser	Phe	Arg	Cys	Val	Gln	Gln	Glu	Asp	Asp	Glu	Ser
305					310					315					320
Gly	Lys	Ile	Gly	Val 325	Суз	Leu	Ser	Lys	Asp 330	Ile	Thr	Asn	Val	Ala 335	Gly
Thr	Thr	Leu	Thr 340	Lys	Asn	Ile	Ala	Thr 345	Leu	Gly	Pro	Leu	Ile 350	Leu	Pro
Leu	Ser	Glu 355	Lys	Phe	Leu	Phe	Phe 360	Ala	Thr	Phe	Val	Ala 365	Lys	Lys	Leu
Leu	Lys 370	Asp	Lys	Ile	Lys	His		Tyr	Val	Pro	Asp 380	Phe	Lys	Leu	Ala
Val		His	Phe	Cvs	Ile	His	Ala	Glv	Glv	Arq		Val	Ile	Asp	Glu
385	1-				390			_	_	395				1-	400
	Glu	Lys	Asn			Leu	Ser	Pro			Val	Glu	Ala		
Ser	Thr	Leu		405 Arg	Phe	Gly	Asn		410 Ser	Ser	Ser	Ser		415 Trp	Tyr
G 3	т.	7. 7	420	- 7	<i>a</i> 3	73 7	T -	425	7	D.C	т.	т.	430	7	T
GLU	ьeu	Ala 435	ıyr	TIE	GLu	Ala	Lys 440	GTÀ	Arg	мet	гла	Lys 445	GTĀ	Asn	тЛа

Ala	Trp 450	Gln	Ile	Ala	Leu	Gly 455	Ser	Gly	Phe	Lys	Cys 460	Asn	Ser	Ala	Val	
Trp		Ala	Leu	Arg	Asn 470	Val	Lys	Ala	Ser	Ala 475		Ser	Pro	Trp	Gln 480	
	Суз	Ile	Asp	Arg		Pro	Val	Lys	Ile		Ser	Asp	Leu	Ser		
Ser	Lvs	Thr	His	485 Val	Gln	Asn	Glv	Ara	490 Ser					495		
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_	_				_	aag Lys						-				48
1				5					10					15		
ctt	ttc	aac	ctt	tgc	ttc	ttt	ccg	tta	acg	gcg	atc	gtc	gcc	gga	aaa	96
Leu	Phe	Asn		Суѕ	Phe	Phe	Pro		Thr	Ala	Ile	Val		Gly	Lys	
			20					25					30			
-						gac	_									144
Ala	Tyr	Arg 35	Leu	Thr	Ile	Asp	Asp 40	Leu	His	His	Leu	Tyr 45	Tyr	Ser	Tyr	
						acc Thr		-				-			_	192
Lea	50	1110	11011	104		55	110	1114	110	Lea	60	1114	1		Val	
++~	aa+	+ aa	~++	at a	+ > 0	2+ 6	~~~	2.00	aaa	999	222	aaa	~++	+ 2.0	ata	240
		_	_			atc Ile	-					_	-			240
65					70					75					80	
gtt	gag	tac	tca	tgc	tac	ctt	cca	cca	acg	cat	tgt	aga	tca	agt	atc	288
Val	Glu	Tyr	Ser	-	Tyr	Leu	Pro	Pro		His	Cys	Arg	Ser		Ile	
				85					90					95		
tcc	aag	gtc	atg	gat	atc	ttt	tat	caa	gta	aga	aaa	gct	gat	cct	tct	336
Ser	Lys	Val	Met 100	Asp	Ile	Phe	Tyr	Gln 105	Val	Arg	Lys	Ala	Asp 110	Pro	Ser	
				_	-	gac	_	_			_		_		_	384
Arg	ASN	115	inr	Cys	Asp	Asp	120	ser	rrp	Leu	Asp	125	Leu	Arg	гуз	
																46.5
		_	_			cta Leu		_	-							432
	130				-	135	-	•			140	-			<u> </u>	
cta	ctt	can	ata	cct	ccc	cgg	aan	act	ttt	aca	aca	aca	cat	gaa	gag	480
y	T 011	Clr	77-1	Dao	Dwo	7 20 27	T 776	The	Dho	71-	אר כ	פרכ	7 20 00	~~~ ~1	C1.,	100

Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu

145 150 155 160

_			_						-		cta Leu		_			528
	-				-						gtg Val			_	_	576
					_				_	_	gtt Val				-	624
	_	_		_	_	_					ggc Gly 220	_		_	_	672
_		-		-		-		-	_	-	ttg Leu	_		-		720
		_		_				_			aac Asn					768
		_		-				_	_	_	tca Ser		-	_		816
_	-			_	-		_				aag Lys			-	_	864
-			-				-		_	-	cga Arg 300	_				912
-	_		_			_	_				gga Gly	_	_			960
					-	-		-	-		acc Thr	-	-	-		1008
_	_	_	_				_	_	_		ccg Pro	_			-	1056
	-							-			atg Met		_			1104
		-							-	_	gat Asp 380				_	1152

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	_			_							agc Ser					1	296
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		_				-		_	_		aat Asn	_			_	1	440
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